

CLEAN COPY OF THE AMENDED AND NEW CLAIMS

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10. (Amended) A transformed Coryneform bacterium comprising an isolated sigH gene having the polynucleotide sequence of SEQ ID NO: 1.

Please add the following new claims:

32. (New) The bacterium of claim 10, wherein said sigH gene is over-expressed.

33. (New) A transformed recombinant coryneform bacterium comprising an increased intracellular concentration or activity of polypeptide having the amino acid sequence of SEQ ID NO: 2, wherein said intracellular concentration or activity is increased by at least 10% over a concentration or activity of a wild type coryneform bacterium.

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34. (New) The coryneform bacterium of claim 33, wherein said intracellular concentration or activity is increased by at least 25 % over the concentration or activity of a wild type coryneform bacterium.

35. (New) The coryneform bacterium of claim 33, wherein said intracellular concentration or activity is increased by at least 50 % over the concentration or activity of a wild type coryneform bacterium.

36. (New) The coryneform bacterium of claim 33, wherein said polypeptide is encoded by an isolated polynucleotide comprising the nucleotide sequence of SEQ ID NO: 1 and said polypeptide is over-expressed.

37. (New) The coryneform bacterium of claim 36, wherein said isolated polynucleotide includes nucleotides 302 to 919 of SEQ ID NO: 1.

38. (New) A transformed coryneform bacterium comprising an isolated polynucleotide encoding a polypeptide comprising the amino acid sequence of SEQ ID NO: 2.

39. (New) The coryneform bacterium of claim 38, wherein said polypeptide is over-expressed to the extent that an intracellular concentration of said polypeptide is increased by at least 10% over a concentration in a wild type coryneform bacterium.

40. (New) The coryneform bacterium of claim 39, wherein said over-expression of said polypeptide is achieved by increasing the copy number of the polynucleotide encoding said polypeptide.

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41. (New) The coryneform bacterium of claim 33, wherein said coryneform bacterium is selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoglutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium thermoaminogenes*, *Corynebacterium melassecola*, *Brevibacterium flavum*, *Brevibacterium lactofermentum*, and *Brevibacterium divaricatum*.

42. (New) The coryneform bacterium of claim 38 wherein said coryneform bacterium is selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoglutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium thermoaminogenes*, *Corynebacterium melassecola*, *Brevibacterium flavum*, *Brevibacterium lactofermentum*, and *Brevibacterium divaricatum*.

43. (New) The coryneform bacterium of claim 33, wherein said coryneform bacterium produces an L-amino acid selected from the group consisting of L-asparagine, L-threonine, L-serine, L-glutamate, L-glycine, L-alanine, L-cysteine, L-valine, L-methionine, L-isoleucine, L-leucine, L-tyrosine, L-phenylalanine, L-histidine, L-lysine, L-tryptophan and L-arginine.

44. (New) The coryneform bacterium of claim 43, wherein said L-amino acid is L-lysine.

45. (New) The coryneform bacterium of claim 34, wherein said coryneform bacterium produces an L-amino acid selected from the group consisting of L-asparagine, L-threonine, L-serine, L-glutamate, L-glycine, L-alanine, L-cysteine, L-valine, L-methionine, L-isoleucine, L-leucine, L-tyrosine, L-phenylalanine, L-histidine, L-lysine, L-tryptophan and L-arginine.

46. (New) The coryneform bacterium of claim 45, wherein said L-amino acid is L-lysine.

47. (New) The coryneform bacterium of claim 41, wherein said coryneform bacterium produces an L-amino acid selected from the group consisting of L-asparagine, L-threonine, L-serine, L-glutamate, L-glycine, L-alanine, L-cysteine, L-valine, L-methionine, L-isoleucine, L-leucine, L-tyrosine, L-phenylalanine, L-histidine, L-lysine, L-tryptophan and L-arginine.

48. (New) The coryneform bacterium of claim 47, wherein said L-amino acid is L-lysine.

49. (New) A transformed coryneform bacterium comprising an over-expressed sigH gene, wherein said sigH gene comprises the nucleotide sequence of SEQ ID NO: 1.

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